

B. Whidmon

# 15108  
10/11/01  
1600

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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/380,546A

DATE: 10/05/2001  
TIME: 13:27:19

Input Set : A:\Wallach23.txt  
Output Set: N:\CRF3\10052001\I380546A.raw

3 <110> APPLICANT: WALLACH, David  
4 GOLTSEV, Yura  
5 KOVALENKO, Andrei  
6 VARFOLOMEEV, Eugene  
7 BRODIANSKI, Vadim  
9 <120> TITLE OF INVENTION: CASH (CASPASE HOMOLOGUE) WITH DEATH EFFECTOR DOMAIN,  
10 MODULATORS OF THE FUNCTION OF FAS RECEPTORS  
12 <130> FILE REFERENCE: WALLACH=23  
14 <140> CURRENT APPLICATION NUMBER: 09/380,546A  
15 <141> CURRENT FILING DATE: 1999-11-29  
17 <150> PRIOR APPLICATION NUMBER: PCT/IL98/00098  
18 <151> PRIOR FILING DATE: 1998-02-26  
20 <150> PRIOR APPLICATION NUMBER: IL 120367  
21 <151> PRIOR FILING DATE: 1997-03-03  
23 <150> PRIOR APPLICATION NUMBER: IL120759  
24 <151> PRIOR FILING DATE: 1997-05-01  
26 <160> NUMBER OF SEQ ID NOS: 20  
28 <170> SOFTWARE: PatentIn Ver. 2.0  
30 <210> SEQ ID NO: 1  
31 <211> LENGTH: 2243  
32 <212> TYPE: DNA  
33 <213> ORGANISM: Homo sapiens  
35 <220> FEATURE:  
36 <221> NAME/KEY: CDS  
37 <222> LOCATION: (482)..(1921)  
39 <400> SEQUENCE: 1  
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44 cacagtggat gcccgtatt ggactttgt ccagtgcacag ctgagacaac aaggaccacg 180  
46 ggaggagggtg taggagagaa ggcgcgcgaaa cagcgatcgc ccagcaccaa gtccgcttcc 240  
48 aggcttcgg tttcttgcc tccatcttgg gtgcgccttc ccggcgtcta ggggagcgaa 300  
50 ggctgagggtg gcagcggcag gagagtccgg ccgcgcacagg acgaactccc ccactggaaa 360  
52 ggattctgaa agaaatgaag tcagccctca gaaatgaagt tgactgcctg ctggcttcc 420  
54 tggactgg cccggagctg tactgcaaga cccttgtgag cttccctagt ctaagagtag 480  
56 g atg tct gct gaa gtc atc cat cag gtt gaa gaa gca ctt gat aca gat 529  
57 Met Ser Ala Glu Val Ile His Gln Val Glu Glu Ala Leu Asp Thr Asp  
58 1 5 10 15  
60 gag aag gag atg ctg ctc ttt ttg tgc cgg gat gtt gct ata gat gtg 577  
61 Glu Lys Glu Met Leu Leu Phe Leu Cys Arg Asp Val Ala Ile Asp Val  
62 20 25 30  
64 gtt cca cct aat gtc agg gac ctt ctg gat att tta cgg gaa aga ggt 625  
65 Val Pro Pro Asn Val Arg Asp Leu Leu Asp Ile Leu Arg Glu Arg Gly  
66 35 40 45  
68 aag ctg tct gtc ggg gac ttg gct gaa ctg ctc tac aga gtg agg cga 673  
69 Lys Leu Ser Val Gly Asp Leu Ala Glu Leu Leu Tyr Arg Val Arg Arg  
70 50 55 60  
72 ttt gac ctg ctc aaa cgt atc ttg aag atg gac aga aaa gct gtg gag 721

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74	65				70					75							80
76	acc	cac	ctg	ctc	agg	aac	cct	cac	ctt	gtt	tgc	gac	tat	aga	gtg	ctg	769
77	Thr	His	Leu	Leu	Arg	Asn	Pro	His	Leu	Val	Ser	Asp	Tyr	Arg	Val	Leu	
78					85					90						95	
80	atg	gca	gag	att	ggt	gag	gat	ttg	gat	aaa	tct	gat	gtg	tcc	tca	tta	817
81	Met	Ala	Glu	Ile	Gly	Glu	Asp	Leu	Asp	Lys	Ser	Asp	Val	Ser	Ser	Leu	
82					100					105						110	
84	att	ttc	ctc	atg	aag	gat	tac	atg	ggc	cga	ggc	aag	ata	agc	aag	gag	865
85	Ile	Phe	Leu	Met	Lys	Asp	Tyr	Met	Gly	Arg	Gly	Lys	Ile	Ser	Lys	Glu	
86					115					120						125	
88	aag	agt	ttc	ttg	gac	ctt	gtg	gtt	gag	ttg	gag	aaa	cta	aat	ttg	gtt	913
89	Lys	Ser	Phe	Leu	Asp	Leu	Val	Val	Glu	Leu	Glu	Lys	Leu	Asn	Leu	Val	
90					130					135						140	
92	gcc	cca	gat	caa	ctg	gat	tta	tta	gaa	aaa	tgc	cta	aag	aac	atc	cac	961
93	Ala	Pro	Asp	Gln	Leu	Asp	Leu	Leu	Glu	Lys	Cys	Leu	Lys	Asn	Ile	His	
94					145					150						160	
96	aga	ata	gac	ctg	aag	aca	aaa	atc	cag	aag	tac	aag	cag	tct	gtt	caa	1009
97	Arg	Ile	Asp	Leu	Lys	Thr	Lys	Ile	Gln	Lys	Tyr	Lys	Gln	Ser	Val	Gln	
98					165					170						175	
100	gga	gca	ggg	aca	agt	tac	agg	aat	gtt	ctc	caa	gca	gca	atc	caa	aag	1057
101	Gly	Ala	Gly	Thr	Ser	Tyr	Arg	Asn	Val	Leu	Gln	Ala	Ala	Ile	Gln	Lys	
102					180					185						190	
104	agt	ctc	aag	gat	cct	tca	aat	aac	ttc	agg	ctc	cat	aat	ggg	aga	agt	1105
105	Ser	Leu	Lys	Asp	Pro	Ser	Asn	Asn	Phe	Arg	Leu	His	Asn	Gly	Arg	Ser	
106					195					200						205	
108	aaa	gaa	caa	aga	ctt	aag	gaa	cag	ctt	ggc	gct	caa	caa	gaa	cca	gtg	1153
109	Lys	Glu	Gln	Arg	Leu	Lys	Glu	Gln	Leu	Gly	Ala	Gln	Gln	Glu	Pro	Val	
110					210					215						220	
112	aag	aaa	tcc	att	cag	gaa	tca	gaa	gct	ttt	ttg	cct	cag	agc	ata	cct	1201
113	Lys	Lys	Ser	Ile	Gln	Glu	Ser	Glu	Ala	Phe	Leu	Pro	Gln	Ser	Ile	Pro	
114					225					230						240	
116	gaa	gag	aga	tac	aag	atg	aag	agc	aag	ccc	cta	gga	atc	tgc	ctg	ata	1249
117	Glu	Glu	Arg	Tyr	Lys	Met	Lys	Ser	Lys	Pro	Leu	Gly	Ile	Cys	Leu	Ile	
118					245					250						255	
120	atc	gat	tgc	att	ggc	aat	gag	aca	gag	ctt	ctt	cga	gac	acc	ttc	act	1297
121	Ile	Asp	Cys	Ile	Gly	Asn	Glu	Thr	Glu	Leu	Leu	Arg	Asp	Thr	Phe	Thr	
122					260					265						270	
124	tcc	ctg	ggc	tat	gaa	gtc	cag	aaa	ttc	ttg	cat	ctc	agt	atg	cat	ggt	1345
125	Ser	Leu	Gly	Tyr	Glu	Val	Gln	Lys	Phe	Leu	His	Leu	Ser	Met	His	Gly	
126					275					280						285	
128	ata	tcc	cag	att	ctt	ggc	caa	ttt	gcc	tgt	atg	ccc	gag	cac	cga	gac	1393
129	Ile	Ser	Gln	Ile	Leu	Gly	Gln	Phe	Ala	Cys	Met	Pro	Glu	His	Arg	Asp	
130					290					295						300	
132	tac	gac	agc	ttt	gtt	tgt	gtc	ctg	gtg	agc	cga	gga	ggc	tcc	cag	agt	1441
133	Tyr	Asp	Ser	Phe	Val	Cys	Val	Leu	Val	Ser	Arg	Gly	Gly	Ser	Gln	Ser	
134					305					310						320	
136	gtg	tat	ggt	gtt	gat	cag	act	cac	tca	ggg	ctc	ccc	ctg	cat	cac	atc	1489
137	Val	Tyr	Gly	Val	Asp	Gln	Thr	His	Ser	Gly	Leu	Pro	Leu	His	His	Ile	

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140	agg agg atg ttc atg gga gat tca tgc cct tat cta gca ggg aag cca			1537
141	Arg Arg Met Phe Met Gly Asp Ser Cys Pro Tyr Leu Ala Gly Lys Pro			
142	340	345	350	
144	aag atg ttt ttt att cag aac tat gtg gtg tca gag ggc cag ctg gag			1585
145	Lys Met Phe Phe Ile Gln Asn Tyr Val Val Ser Glu Gly Gln Leu Glu			
146	355	360	365	
148	aac agc agc ctc ttg gag gtg gat ggg cca gcg atg aag aat gtg gaa			1633
149	Asn Ser Ser Leu Leu Glu Val Asp Gly Pro Ala Met Lys Asn Val Glu			
150	370	375	380	
152	ttc aag gct cag aag cga ggg ctg tgc aca gtt cac cga gaa gct gac			1681
153	Phe Lys Ala Gln Lys Arg Gly Leu Cys Thr Val His Arg Glu Ala Asp			
154	385	390	395	400
156	ttc ttc tgg agc ctg tgt act gcg gac atg tcc ctg ctg gag cag tct			1729
157	Phe Phe Trp Ser Leu Cys Thr Ala Asp Met Ser Leu Leu Glu Gln Ser			
158	405	410	415	
160	cac agc tca ccg tcc ctg tac ctg cag tgc ctc tcc cag aaa ctg aga			1777
161	His Ser Ser Pro Ser Leu Tyr Leu Gln Cys Leu Ser Gln Lys Leu Arg			
162	420	425	430	
164	caa gaa aga aaä cgc cca ctc ctg gat ctt cac att gaa ctc aat ggc			1825
165	Gln Glü Arg Lys Arg Pro Leu Leu Asp Leu His Ile Glu Leu Asn Gly			
166	435	440	445	
168	tac atg tat gat tgg aac agc aga gtt tct gcc aag gag aaa tat tat			1873
169	Tyr Met Tyr Asp Trp Asn Ser Arg Val Ser Ala Lys Glu Lys Tyr Tyr			
170	450	455	460	
172	gtc tgg ctg cag cac act ctg aga aag aaa ctt atc ctc tcc tac aca			1921
173	Val Trp Leu Gln His Thr Leu Arg Lys Lys Leu Ile Leu Ser Tyr Thr			
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176	taagaaacca aaaggctggg cgttagtgct cacacctgta atccccagcac tttggggaggc			1981
178	caaggagggc agatcacttc aggtcaggag ttgcagacca gcctggccaa catggtaaac			2041
180	gtctgtcccta gtaaaaatgc aaaaattagc tgggtgtggg tgggtgtacc tgggttccca			2101
182	gttacttggg aggctgaggt gggaggatct ttgttacccca ggagttcagg gtcatacat			2161
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198	Glu Lys Glu Met Leu Leu Phe Leu Cys Arg Asp Val Ala Ile Asp Val			
199	20	25	30	
201	Val Pro Pro Asn Val Arg Asp Leu Leu Asp Ile Leu Arg Glu Arg Gly			
202	35	40	45	
204	Lys Leu Ser Val Gly Asp Leu Ala Glu Leu Leu Tyr Arg Val Arg Arg			
205	50	55	60	
207	Phe Asp Leu Leu Lys Arg Ile Leu Lys Met Asp Arg Lys Ala Val Glu			
208	65	70	75	80

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210 Thr His Leu Leu Arg Asn Pro His Leu Val Ser Asp Tyr Arg Val Leu  
 211 85 90 95  
 213 Met Ala Glu Ile Gly Glu Asp Leu Asp Lys Ser Asp Val Ser Ser Leu  
 214 100 105 110  
 216 Ile Phe Leu Met Lys Asp Tyr Met Gly Arg Gly Lys Ile Ser Lys Glu  
 217 115 120 125  
 219 Lys Ser Phe Leu Asp Leu Val Val Glu Leu Glu Lys Leu Asn Leu Val  
 220 130 135 140  
 222 Ala Pro Asp Gln Leu Asp Leu Leu Glu Lys Cys Leu Lys Asn Ile His  
 223 145 150 155 160  
 225 Arg Ile Asp Leu Lys Thr Lys Ile Gln Lys Tyr Lys Gln Ser Val Gln  
 226 165 170 175  
 228 Gly Ala Gly Thr Ser Tyr Arg Asn Val Leu Gln Ala Ala Ile Gln Lys  
 229 180 185 190  
 231 Ser Leu Lys Asp Pro Ser Asn Asn Phe Arg Leu His Asn Gly Arg Ser  
 232 195 200 205  
 234 Lys Glu Gln Arg Leu Lys Glu Gln Leu Gly Ala Gln Gln Glu Pro Val  
 235 210 215 220  
 237 Lys Lys Ser Ile Gln Glu Ser Glu Ala Phe Leu Pro Gln Ser Ile Pro  
 238 225 230 235 240  
 240 Glu Glu Arg Tyr Lys Met Lys Ser Lys Pro Leu Gly Ile Cys Leu Ile  
 241 245 250 255  
 243 Ile Asp Cys Ile Gly Asn Glu Thr Glu Leu Leu Arg Asp Thr Phe Thr  
 244 260 265 270  
 246 Ser Leu Gly Tyr Glu Val Gln Lys Phe Leu His Leu Ser Met His Gly  
 247 275 280 285  
 249 Ile Ser Gln Ile Leu Gly Gln Phe Ala Cys Met Pro Glu His Arg Asp  
 250 290 295 300  
 252 Tyr Asp Ser Phe Val Cys Val Leu Val Ser Arg Gly Gly Ser Gln Ser  
 253 305 310 315 320  
 255 Val Tyr Gly Val Asp Gln Thr His Ser Gly Leu Pro Leu His His Ile  
 256 325 330 335  
 258 Arg Arg Met Phe Met Gly Asp Ser Cys Pro Tyr Leu Ala Gly Lys Pro  
 259 340 345 350  
 261 Lys Met Phe Phe Ile Gln Asn Tyr Val Val Ser Glu Gly Gln Leu Glu  
 262 355 360 365  
 264 Asn Ser Ser Leu Leu Glu Val Asp Gly Pro Ala Met Lys Asn Val Glu  
 265 370 375 380  
 267 Phe Lys Ala Gln Lys Arg Gly Leu Cys Thr Val His Arg Glu Ala Asp  
 268 385 390 395 400  
 270 Phe Phe Trp Ser Leu Cys Thr Ala Asp Met Ser Leu Leu Glu Gln Ser  
 271 405 410 415  
 273 His Ser Ser Pro Ser Leu Tyr Leu Gln Cys Leu Ser Gln Lys Leu Arg  
 274 420 425 430  
 276 Gln Glu Arg Lys Arg Pro Leu Leu Asp Leu His Ile Glu Leu Asn Gly  
 277 435 440 445  
 279 Tyr Met Tyr Asp Trp Asn Ser Arg Val Ser Ala Lys Glu Lys Tyr Tyr  
 280 450 455 460  
 282 Val Trp Leu Gln His Thr Leu Arg Lys Leu Ile Leu Ser Tyr Thr

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293	<222>	LOCATION:	(482)..(1144)				
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298	ctcaccgacg	agtctcaact	aaaagggact	cccgagacta	gggggtgggg	ctccgcctca	120
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304	aggcttcgg	tttcttgcc	tccatcttgg	gtgcgccttc	ccggcgctta	ggggagcgaa	300
306	ggctgaggtg	gcagcggcag	gagagtccgg	ccgcgcacagg	acgaactccc	ccactggaaa	360
308	ggattctgaa	agaaatgaag	tcagccctca	gaaatgaagt	tgactgcctg	ctggcttcc	420
310	tgttgactgg	cccgagctg	tactgcaaga	ccctgtgag	cttccctagt	ctaagagtag	480
312	g atg tct	gct gaa gtc	atc cat cag	gtt gaa gaa	gca ctt gat	aca gat	529
313	Met Ser Ala	Glu Val Ile His	Gln Val Glu Ala	Glu Leu Asp Thr	Asp		
314	1	5	10	15			
316	gag aag gag atg	ctg ctc ttt ttg	tgc cg	gat gtt gct	ata gat gtg		577
317	Glu Lys	Glu Met Leu Leu Phe	Leu Cys Arg Asp	Val Ala Ile Asp	Val		
318	20	25	30				
320	gtt cca cct aat	gtc agg gac	ctt ctg	gat att tta	cg	gaa aga ggt	625
321	Val Pro Pro Asn	Val Arg Asp	Leu Leu Asp	Ile Leu Arg	Glu Arg Gly		
322	35	40	45				
324	aag ctg tct	gtc ggg gac	ttg gct	gaa ctg ctc	tac aga	gtg agg cga	673
325	Lys Leu Ser Val	Gly Asp	Leu Ala Glu	Leu Leu Tyr	Arg Val Arg	Arg	
326	50	55	60				
328	ttt gac ctg ctc	aaa cgt atc	ttg aag atg	gac aga	aaa gct	gtg gag	721
329	Phe Asp Leu Leu Lys	Arg Ile Leu Lys	Met Asp Arg	Lys Ala Val	Glu		
330	65	70	75	80			
332	acc cac ctg ctc	agg aac cct	cac ctt	gtt tcg	gac tat	aga gtg ctg	769
333	Thr His Leu Leu Arg	Asn Pro His	Leu Val Ser	Asp Tyr Arg	Val	Leu	
334	85	90	95				
336	atg gca gag att	ggg gag gat	ttg gat	aaa tct	gat gtg	tcc tca tta	817
337	Met Ala Glu Ile	Gly Glu Asp	Leu Asp Lys	Ser Asp Val	Ser Ser	Leu	
338	100	105	110				
340	att ttc ctc atg	aag gat tac	atg ggc	cga ggc	aag ata	agc aag gag	865
341	Ile Phe Leu Met	Lys Asp Tyr	Met Gly Arg	Gly Lys Ile	Ser Lys	Glu	
342	115	120	125				
344	aag agt ttc ttg	gac ctt	gtg gtt	gag ttg	gag aaa	cta aat ttg	913
345	Lys Ser Phe Leu Asp	Leu Val Val	Glu Leu Glu	Lys Leu Asn	Leu Val		
346	130	135	140				
348	gcc cca gat caa	ctg gat	tta tta	gaa aaa	tgc cta	aag aac atc cac	961
349	Ala Pro Asp Gln	Leu Asp Leu	Glu Lys Cys	Leu Lys Asn	Ile His		
350	145	150	155	160			
352	aga ata gac ctg	aag aca aaa	atc cag	aag tac	aag cag	tct gtt caa	1009
353	Arg Ile Asp Leu	Lys Thr	Ile Gln	Lys Tyr	Lys Gln	Ser Val Gln	

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